



SEQUENCE LISTING

<110> Targan, Stephan R.
Vasiliauskas, Eric A.
Mow, William S.
Yang, Huiying
Fleshner, Phillip R.
Rotter, Jerome I.

<120> Methods of Assessing Crohn's Disease
Patient Phenotype by I2, OmpC and ASCA Serologic Response

<130> 66783-142

<140> US 10/723,164

<141> 2003-11-26

<150> US 10/413,501

<151> 2003-04-11

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<213> P. aeruginosa

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<221> CDS

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Phe Lys Ser Lys Asp Glu Ile Leu Arg Ala Val Met Glu Glu Thr Ile
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cat tac aac acc gcg atg atg cgc gct tca ctg gag gag gcg agc acg 145
His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Glu Ala Ser Thr
35 40 45

gtg cgc gaa cgc gtg ctg gcg ctg atc cgc tgc gag ttg cag tcg atc 193
Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile
50 55 60

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Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg
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tcg ctg tcg gcc gaa ggc cag gcg cac gtg ctg gcc ctg cgt gac gtg 289
Ser Leu Ser Ala Glu Gly Gln Ala His Val Leu Ala Leu Arg Asp Val
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Tyr Glu Gln Ile
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<213> P. aeruginosa

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His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Glu Ala Ser Thr
35 40 45
Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile
50 55 60
Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg
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Ser Leu Ser Ala Glu Gly Gln Ala His Val Leu Ala Leu Arg Asp Val
85 90 95
Tyr Glu Gln Ile
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aaagttcaaa gaccttcaga actggcccca gctcctccct ctccacctga tctccccaag 180
aaaactgcag gatagactct gaagcttacc tgagccacct caagctctgg tgatcaccca 240
aggcttcagc cagggcctgg gccccctcgt cccccactct gttgccccag aatctgaaaa 300
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gcctcactgg ggctcctggg cccagcaaaag tggacctgcc tccatctttt ggggtgggatg 480
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cactctggga ttgagtggc ctgcccctct ggctgggact gcagagggag gaggactgtt 180
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atttctaccc cacaatgtta ggcaatggag taaggaaaaa agaccattgg atttcaagag 480
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aaaattctgc cattcctctc tcccgtcacc ccattttaca gatagaaaaa ctgagggttcg 180
gagagctaaa acaggcctgc ccaggggcct taccagactt ccaggatggg gtcattcctt 240
tcaagggggc tgcaggaggg cttctgcccc taggtagggt atgcagttat tggacaacct 300
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gttaaagaga ctgcaggagt tagccagtct actgaagccc acctgtccct tagacacatc 420
ctgctcatgt ctgagattcc caatgagctc atcaacaaag gctcagtacc atcagtgaaa 480
tgtaaccgtc tctcttccat tccactagat agtttatcaa attaagtagc cactccctta 540
g 541
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ggatgtgtct aaggacaggg tgggcttcag tagactggct aactcctgca gtctctttaa 180
ctggacagtt tcaagaggaa aaccaagaat ccttgaagct caccattgta tcttcttttc 240
caggttgtcc aataactgca tcacctacct aggggcagaa gccctcctgc aggccccctg 300
aaaggaatga caccatcctg gaagtctggg aaggcccctg ggcaggcctg ttttagctct 360
ccgaacctca gtttttctat ctgtaaaatg ggggtgacggg agagaggaat ggcagaattt 420
tgaggatccc ttctgattct gacattcagt gagaatgatt ctgcatgtga aggatctgat 480
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1 5 10 15

ggc gca gca aac gct gct gaa gtt tac aac aaa gac ggc aac aaa tta 96
Gly Ala Ala Asn Ala Ala Glu Val Tyr Asn Lys Asp Gly Asn Lys Leu
20 25 30

gat ctg tac ggt aaa gta gac ggc ctg cac tat ttc tct gac aac aaa 144
Asp Leu Tyr Gly Lys Val Asp Gly Leu His Tyr Phe Ser Asp Asn Lys
35 40 45

gat gta gat ggc gac cag acc tac atg cgt ctt ggc ttc aaa ggt gaa 192
Asp Val Asp Gly Asp Gln Thr Tyr Met Arg Leu Gly Phe Lys Gly Glu
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act cag gtt act gac cag ctg acc ggt tac ggc cag tgg gaa tat cag			240
Thr Gln Val Thr Asp Gln Leu Thr Gly Tyr Gly Gln Trp Glu Tyr Gln			
65	70	75	80
atc cag ggc aac agc gct gaa aac gaa aac aac tcc tgg acc cgt gtg			288
Ile Gln Gly Asn Ser Ala Glu Asn Glu Asn Asn Ser Trp Thr Arg Val			
	85	90	95
gca ttc gca ggt ctg aaa ttc cag gat gtg ggt tct ttc gac tac ggt			336
Ala Phe Ala Gly Leu Lys Phe Gln Asp Val Gly Ser Phe Asp Tyr Gly			
	100	105	110
cgt aac tac ggc gtt gtt tat gac gta act tcc tgg acc gac gta ctg			384
Arg Asn Tyr Gly Val Val Tyr Asp Val Thr Ser Trp Thr Asp Val Leu			
	115	120	125
cca gaa ttc ggt ggt gac acc tac ggt tct gac aac ttc atg cag cag			432
Pro Glu Phe Gly Gly Asp Thr Tyr Gly Ser Asp Asn Phe Met Gln Gln			
	130	135	140
cgt ggt aac ggc ttc gcg acc tac cgt aac act gac ttc ttc ggt ctg			480
Arg Gly Asn Gly Phe Ala Thr Tyr Arg Asn Thr Asp Phe Phe Gly Leu			
145	150	155	160
gtt gac ggc ctg aac ttt gct gtt cag tac cag ggt aaa aac ggc aac			528
Val Asp Gly Leu Asn Phe Ala Val Gln Tyr Gln Gly Lys Asn Gly Asn			
	165	170	175
cca tct ggt gaa ggc ttt act agt ggc gta act aac aac ggt cgt gac			576
Pro Ser Gly Glu Gly Phe Thr Ser Gly Val Thr Asn Asn Gly Arg Asp			
	180	185	190
gca ctg cgt caa aac ggc gac ggc gtc ggc ggt tct atc act tat gat			624
Ala Leu Arg Gln Asn Gly Asp Gly Val Gly Gly Ser Ile Thr Tyr Asp			
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Tyr Glu Gly Phe Gly Ile Gly Gly Ala Ile Ser Ser Ser Lys Arg Thr			
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Asp Ala Gln Asn Thr Ala Ala Tyr Ile Gly Asn Gly Asp Arg Ala Glu			
225	230	235	240
acc tac act ggt ggt ctg aaa tac gac gct aac aac atc tac ctg gct			768
Thr Tyr Thr Gly Gly Leu Lys Tyr Asp Ala Asn Asn Ile Tyr Leu Ala			
	245	250	255
gct cag tac acc cag acc tac aac gca act cgc gta ggt tcc ctg ggt			816
Ala Gln Tyr Thr Gln Thr Tyr Asn Ala Thr Arg Val Gly Ser Leu Gly			
	260	265	270

tgg gcg aac aaa gca cag aac ttc gaa gct gtt gct cag tac cag ttc	864
Trp Ala Asn Lys Ala Gln Asn Phe Glu Ala Val Ala Gln Tyr Gln Phe	
275 280 285	
gac ttc ggt ctg cgt ccg tcc ctg gct tac ctg cag tct aaa ggt aaa	912
Asp Phe Gly Leu Arg Pro Ser Leu Ala Tyr Leu Gln Ser Lys Gly Lys	
290 295 300	
aac ctg ggt cgt ggc tac gac gac gaa gat atc ctg aaa tat gtt gat	960
Asn Leu Gly Arg Gly Tyr Asp Asp Glu Asp Ile Leu Lys Tyr Val Asp	
305 310 315 320	
gtt ggt gct acc tac tac ttc aac aaa aac atg tcc acc tac gtt gac	1008
Val Gly Ala Thr Tyr Tyr Phe Asn Lys Asn Met Ser Thr Tyr Val Asp	
325 330 335	
tac aaa atc aac ctg ctg gac gac aac cag ttc act cgt gac gct ggc	1056
Tyr Lys Ile Asn Leu Leu Asp Asp Asn Gln Phe Thr Arg Asp Ala Gly	
340 345 350	
atc aac act gat aac atc gta gct ctg ggt ctg gtt tac cag ttc	1101
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355 360 365	

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Asp Leu Tyr Gly Lys Val Asp Gly Leu His Tyr Phe Ser Asp Asn Lys	
35 40 45	
Asp Val Asp Gly Asp Gln Thr Tyr Met Arg Leu Gly Phe Lys Gly Glu	
50 55 60	
Thr Gln Val Thr Asp Gln Leu Thr Gly Tyr Gly Gln Trp Glu Tyr Gln	
65 70 75 80	
Ile Gln Gly Asn Ser Ala Glu Asn Glu Asn Asn Ser Trp Thr Arg Val	
85 90 95	
Ala Phe Ala Gly Leu Lys Phe Gln Asp Val Gly Ser Phe Asp Tyr Gly	
100 105 110	
Arg Asn Tyr Gly Val Val Tyr Asp Val Thr Ser Trp Thr Asp Val Leu	
115 120 125	
Pro Glu Phe Gly Gly Asp Thr Tyr Gly Ser Asp Asn Phe Met Gln Gln	
130 135 140	
Arg Gly Asn Gly Phe Ala Thr Tyr Arg Asn Thr Asp Phe Phe Gly Leu	
145 150 155 160	

Val	Asp	Gly	Leu	Asn	Phe	Ala	Val	Gln	Tyr	Gln	Gly	Lys	Asn	Gly	Asn	
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Pro	Ser	Gly	Glu	Gly	Phe	Thr	Ser	Gly	Val	Thr	Asn	Asn	Gly	Arg	Asp	
			180					185					190			
Ala	Leu	Arg	Gln	Asn	Gly	Asp	Gly	Val	Gly	Gly	Ser	Ile	Thr	Tyr	Asp	
		195					200					205				
Tyr	Glu	Gly	Phe	Gly	Ile	Gly	Gly	Ala	Ile	Ser	Ser	Ser	Lys	Arg	Thr	
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Asp	Ala	Gln	Asn	Thr	Ala	Ala	Tyr	Ile	Gly	Asn	Gly	Asp	Arg	Ala	Glu	
225					230				235					240		
Thr	Tyr	Thr	Gly	Gly	Leu	Lys	Tyr	Asp	Ala	Asn	Asn	Ile	Tyr	Leu	Ala	
			245					250						255		
Ala	Gln	Tyr	Thr	Gln	Thr	Tyr	Asn	Ala	Thr	Arg	Val	Gly	Ser	Leu	Gly	
		260						265				270				
Trp	Ala	Asn	Lys	Ala	Gln	Asn	Phe	Glu	Ala	Val	Ala	Gln	Tyr	Gln	Phe	
	275					280						285				
Asp	Phe	Gly	Leu	Arg	Pro	Ser	Leu	Ala	Tyr	Leu	Gln	Ser	Lys	Gly	Lys	
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305					310					315				320		
Val	Gly	Ala	Thr	Tyr	Tyr	Phe	Asn	Lys	Asn	Met	Ser	Thr	Tyr	Val	Asp	
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Tyr	Lys	Ile	Asn	Leu	Leu	Asp	Asp	Asn	Gln	Phe	Thr	Arg	Asp	Ala	Gly	
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